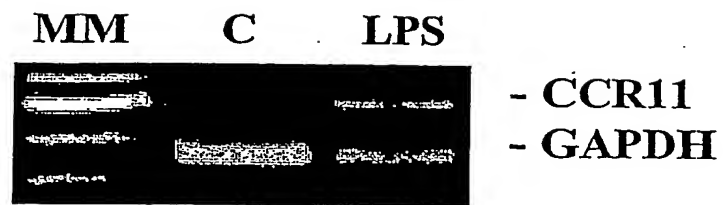


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CELLS

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Fig. 1

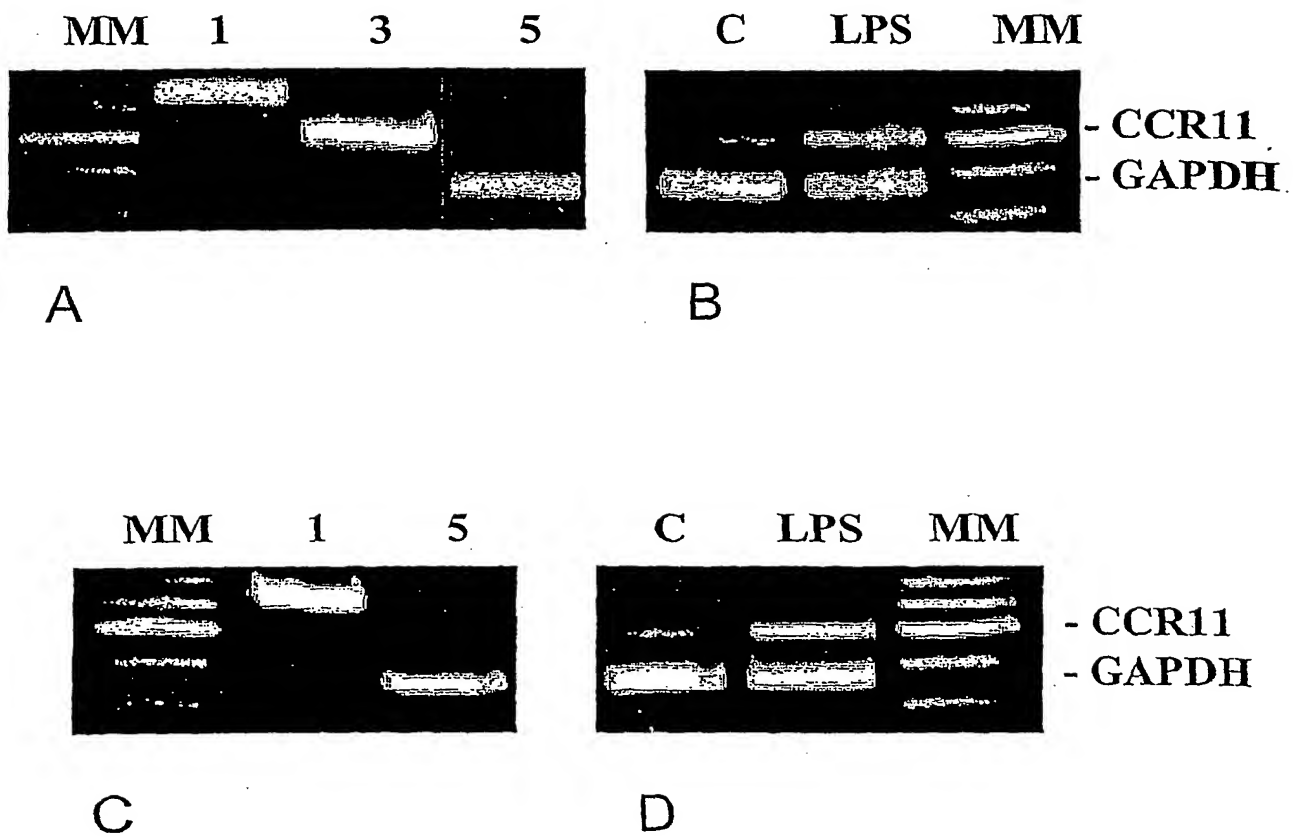


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Fig. 2

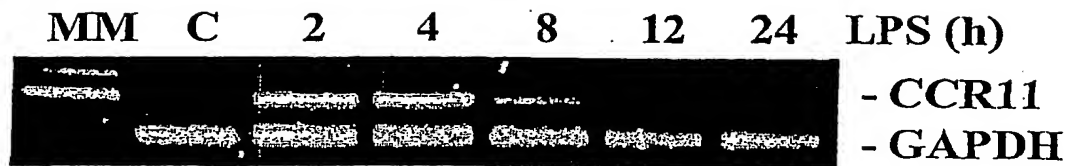


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Fig. 3

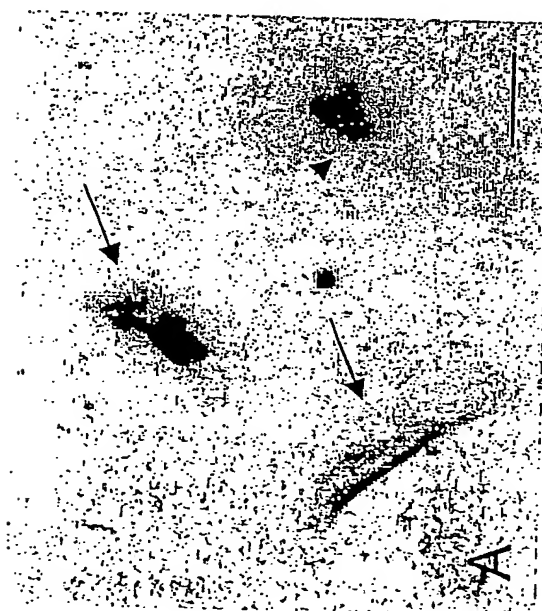
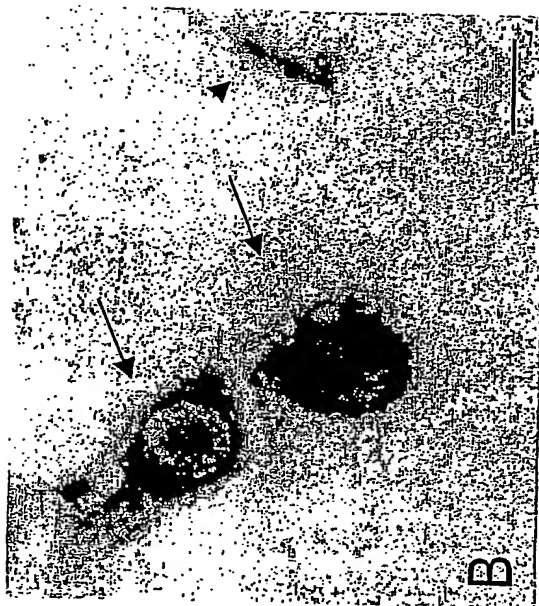


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Fig. 4

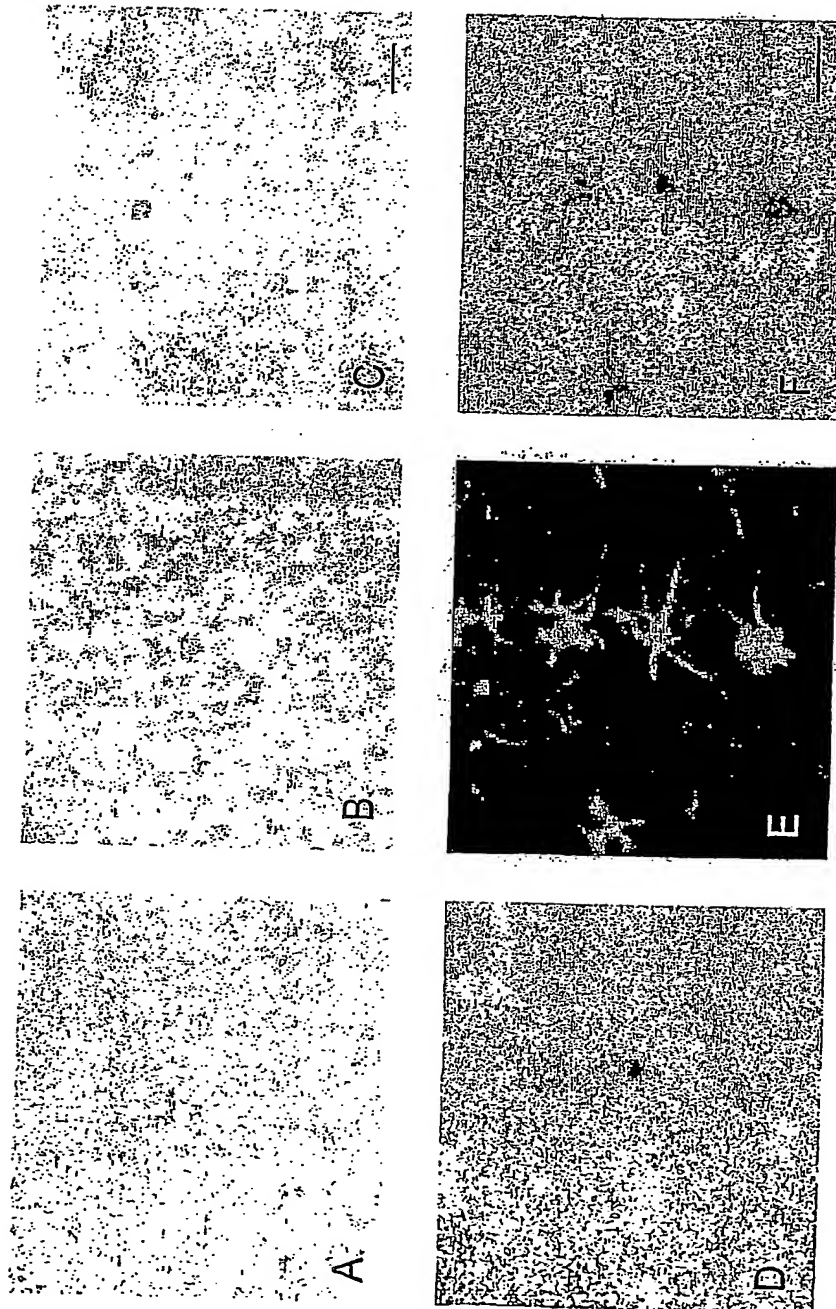


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Fig. 5

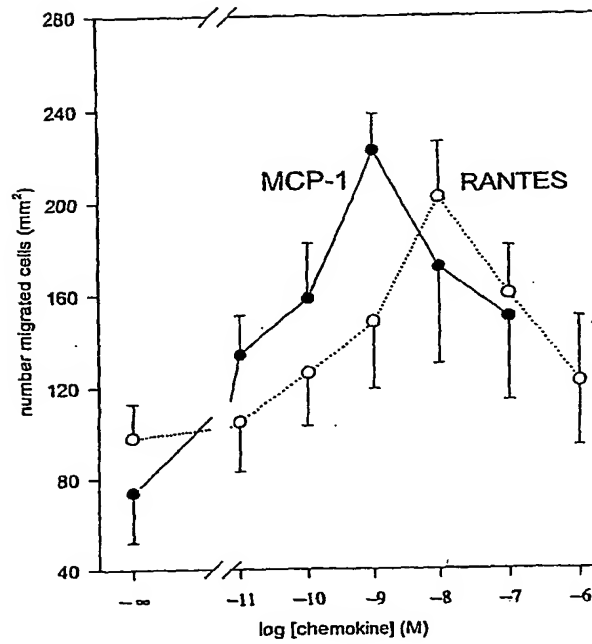


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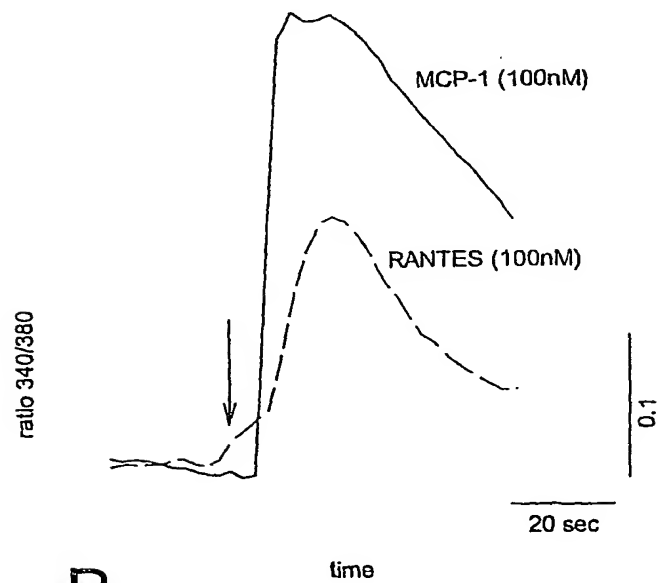
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Fig. 6.



A



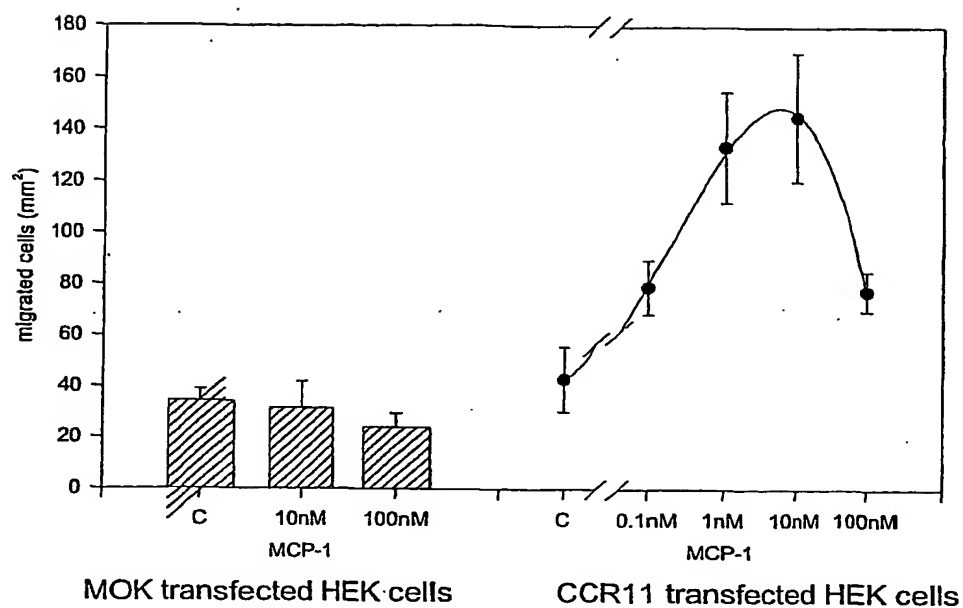
B

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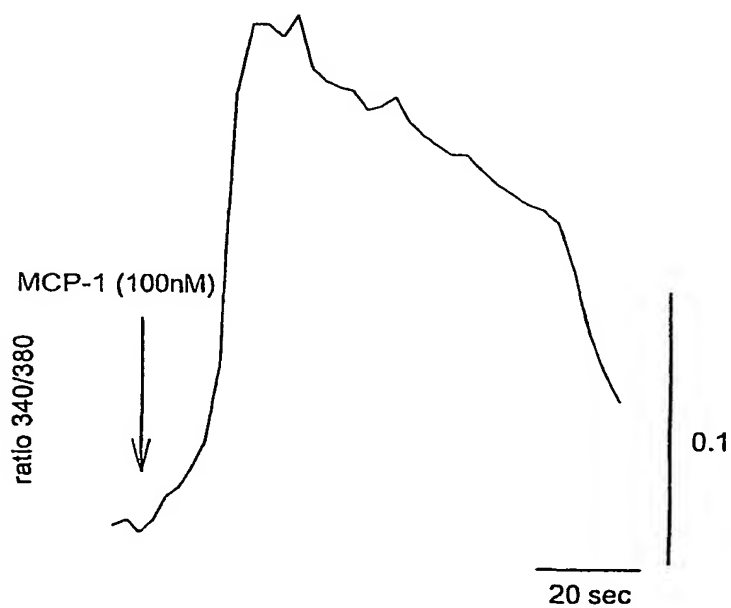
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Fig. 7



A



B

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Fig. 8

CLUSTAL W (1.81) multiple sequence alignment

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hCCR12      ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCAT---AGAAGGTGAA 57
mCCR12      ATGGATAACTACACAGTGGCCCCGGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
          **** * * * * * **** * * * * * **** * * * * *
hCCR12      CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGAGCGCCAGGCACCTCTCAGCCCGAG 117
mCCR12      CTGGACAACAGTGGGCGGACCAA-GTTCCG-----GCCCCGAGTTCCTCTCCCCCCAG 114
          **** * * * * * **** * * * * * **** * * * * *
hCCR12      CTGGTGCCATCAGTCTGCTCTGCTGTGTGTTGTGATCGGTGTCTCTGGACAATCTCCTGGTT 177
mCCR12      CAGGTGCTGCAGTTCCTGCTGCGCGGTGTTTTCGGTGGGTCTCTTGGACAACGTGCTGGCG 174
          * * * * * * * * * * * * * * * * * * * * * * * *
hCCR12      GTGCTTATCCTGGTAAATATAAAGGACTCAAACGCGTGGAAATATCTATCTTCTAAAC 237
mCCR12      GTGTTTATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTCTAAAC 234
          *** * * * * * * * * * * * * * * * * * * * * *
hCCR12      TTGGCAGTTTCTAACTTGTTGTTTCTTGCTTACCCGCGCTTCTGGGCTCATGCTG----- 292
mCCR12      CTGGCACTTTCAAAACCTGTGTGTTTCTGCTTCCCGTGGCGTCTGGGCCCATCTGCAGCA 294
          **** * * * * * * * * * * * * * * * * * * * *
hCCR12      ---GGGGCGATCCC-----ATGTGTAAATTCATTTGGACTGTACTTCGTGGGC 339
mCCR12      CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCTGTGCGACTCCACTCCTCGGGC 354
          *** * * * * * * * * * * * * * * * * * * * *
hCCR12      CTGTACAGTGAGACATTTTCAATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTG 399
mCCR12      TTATACAGCGAGGTGTTTTCACAATCCTCCTCCTGTGCAAGGATACAGGTGTTT-- 412
          * * * * * * * * * * * * * * * * * * * * *
hCCR12      CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTGTC 459
mCCR12      CCCAAGGCGACTGGC-CTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGGGTGCATC 471
          * * * * * * * * * * * * * * * * * * * * *

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Fig. 8a

hCCR12	CTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCCTGAATTGGTGGTTTATAAACCTCAG	519
mCCR12	CTGGCATGGGCCATGGCTACTGCGCTCTCTTTGCCGAGTCTGTGTTTTATGAGCCTCGG	531
	***** * * * * * ***** * * * * * ***** * * * * *	
hCCR12	ATGGAAGACCCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAG	579
mCCR12	ATGGAAGACACAGAAACACAAGTGTGCCTTTGGCAAACTCTACTTCTTGCCAATCGAAGCG	591
	***** ***** * * * * * ***** * * * * * ***** * * * *	
hCCR12	ACATTCTGGAAGCATTTCTGACTTTAAAAAATGAACATTTGGGTCTTGTCTCCTCCCCCTA	639
mCCR12	CCGCTCTGGAAGTACGTTCTGACGTCRAAAATGATCATCTTGGTACTTGTCTTTCTCTIG	651
	* ***** * ***** * ***** * * * * * ***** * * * *	
hCCR12	TTTATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGG	699
mCCR12	CTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAAAGGCAGAGCTTCAGGGAGAGACAG	711
	* ***** * * * * * ***** * * * * * ***** * * * *	
hCCR12	TATAGCCTTTTCAAGCTTGTTTTGGCGTAATGGTAGTCTCTCTCTGATGTGGGCGCC	759
mCCR12	TACGACCTCCACAAGCCGGCTCTTTGTGTCATAACGGGCGTGTCTCTTTGATGTGGGCGCT	771
	** ***** * * * * * ***** * * * * * ***** *****	
hCCR12	TACAAATATGCAATTTTCCGTGCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAG	819
mCCR12	TACAACACTGTGCTTTTCCGTCTGTCTTCCAGGAACACTTGTCCCTGCAGGATGAGAAG	831
	***** * * * * * ***** * * * * * ***** * * * *	
hCCR12	AGCAGGTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACCCTGTC	879
mCCR12	AGCAGTACCACCTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACCCACCCTGTC	891
	***** * * * * * ***** * * * * * ***** *****	
hCCR12	TGCATCAACCCCTCTCCTGTATGCGTTTCTTGATGGGA---CATTTAGCAATACCTCTGC	936
mCCR12	TGCGTCAACCCCGCTGCTCTATTGTCTTCTTGACCGGAGGCCCTTTATGAGATACCTTCGC	951
	*** ***** * * * * * ***** * * * * * ***** * * * *	

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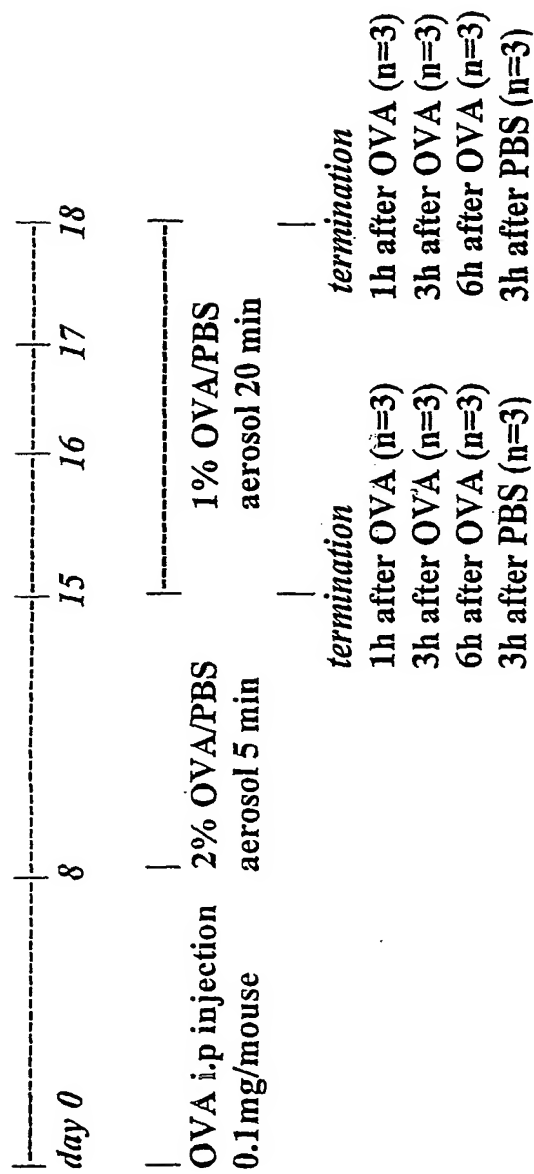
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Fig. 8b

hCCR12	CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC	996
mCCR12	AGCCTGTTCCTCCACGGTGCATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG	1011
	** **** * * * * * * * * * * * * * * *	
hCCR12	ACATCGAGGGAAGAACCTGACCATTCCACCGAAGTGTA	1035
mCCR12	CCTCCAAGGGAAGGTGATGGCAGGCCCATTTGAACGTGACAGCAATTGCATCAAGGCAG	1071
	* * ***** * * * * * * * * * * *	
hCCR12	-----	
mCCR12	GATATAATATAA	1083

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Fig. 9

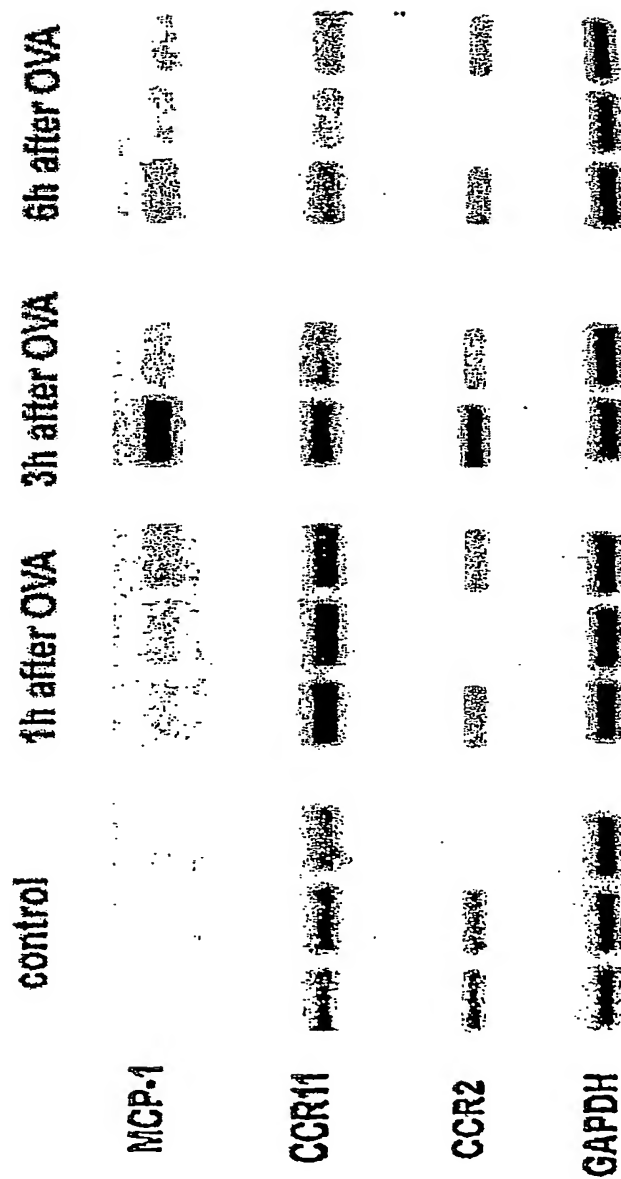


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Fig. 10



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Fig. 11

